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RAW SEQUENCE LISTING   DATE: 06/20/2002
PATENT APPLICATION: US/10/076,416   TIME: 17:39:04

        Input Set : A:\EP.txt
        Output Set: N:\CRF3\06202002\J076416.raw

   3 <110> APPLICANT: RIEPING, Mechthild
   4   THIERBACH, Georg
   6 <120> TITLE OF INVENTION: Process for the fermentative preparation of L-amino acids
using strains
   7   of the Enterobacteriaceae family.
   9 <130> FILE REFERENCE: 218162US0X
  11 <140> CURRENT APPLICATION NUMBER: 10/076,416
  12 <141> CURRENT FILING DATE: 2002-02-19
  14 <150> PRIOR APPLICATION NUMBER: DE 10112107.5
  15 <151> PRIOR FILING DATE: 2001-03-14
  17 <150> PRIOR APPLICATION NUMBER: US 09/987541
  18 <151> PRIOR FILING DATE: 2001-11-15
  20 <150> PRIOR APPLICATION NUMBER: US 60/283612
  21 <151> PRIOR FILING DATE: 2000-04-16
  23 <150> PRIOR APPLICATION NUMBER: US 60/248210
  24 <151> PRIOR FILING DATE: 2000-11-15
  26 <160> NUMBER OF SEQ ID NOS: 12
  28 <170> SOFTWARE: PatentIn version 3.1
  30 <210> SEQ ID NO: 1
  31 <211> LENGTH: 1719
  32 <212> TYPE: DNA
  33 <213> ORGANISM: Escherichia coli
  35 <220> FEATURE:
  36 <221> NAME/KEY: CDS
  37 <222> LOCATION: (1)..(1716)
  38 <223> OTHER INFORMATION:
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  44 1   5   10   15
  46 ggg gtg aaa cgc atc tgg gga gtc aca ggc gac tct ctg aac ggt ctt   96
  47 Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu
  48   20   25   30
  50 agt gac agt ctt aat cgc atg ggc acc atc gag tgg atg tcc acc cgc   144
  51 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg
  52   35   40   45
  54 cac gaa gaa gtg gcg gcc ttt gcc gct ggc gct gaa gca caa ctt agc   192
  55 His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser
  56   50   55   60
  58 gga gaa ctg gcg gtc tgc gcc gga tcg tgc ggc ccc ggc aac ctg cac   240
  59 Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His
  60 65   70   75   80
  62 tta atc aac ggc ctg ttc gat tgc cac cgc aat cac gtt ccg gta ctg   288
  63 Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu

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64              85               90               95
66  gcg att gcc gct cat att ccc tcc agc gaa att ggc agc ggc tat ttc    336
67  Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe
68             100              105              110
70  cag gaa acc cac cca caa gag cta ttc cgc gaa tgt agt cac tat tgc    384
71  Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys
72             115              120              125
74  gag ctg gtt tcc agc ccg gag cag atc cca caa gta ctg gcg att gcc    432
75  Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala
76        130              135              140
78  atg cgc aaa gcg gtg ctt aac cgt ggc gtt tcg gtt gtc gtg tta cca    480
79  Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro
80  145              150              155              160
82  ggc gac gtg gcg tta aaa cct gcg cca gaa ggg gca acc atg cac tgg    528
83  Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp
84             165              170              175
86  tat cat gcg cca caa cca gtc gtg acg ccg gaa gaa gaa gag tta cgc    576
87  Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg
88             180              185              190
90  aaa ctg gcg caa ctg ctg cgt tat tcc agc aat atc gcc ctg atg tgt    624
91  Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys
92        195              200              205
94  ggc agc ggc tgc gcg ggg gcg cat aaa gag tta gtt gag ttt gcc ggg    672
95  Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly
96        210              215              220
98  aaa att aaa gcg cct att gtt cat gcc ctg cgc ggt aaa gaa cat gtc    720
99  Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val
100 225              230              235              240
102 gaa tac gat aat ccg tat gat gtt gga atg acc ggg tta atc ggc ttc    768
103 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe
104             245              250              255
106 tcg tca ggt ttc cat acc atg atg aac gcc gac acg tta gtg cta ctc    816
107 Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu
108        260              265              270
110 ggc acg caa ttt ccc tac cgc gcc ttc tac ccg acc gat gcc aaa atc    864
111 Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile
112        275              280              285
114 att cag att gat atc aac cca gcc agc atc ggc gct cac agc aag gtg    912
115 Ile Gln Ile Asp Ile Asn Pro Ala Ser Ile Gly Ala His Ser Lys Val
116        290              295              300
118 gat atg gca ctg gtc ggc gat atc aag tcg act ctg cgt gca ttg ctt    960
119 Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu
120 305              310              315              320
122 cca ttg gtg gaa gaa aaa gcc gat cgc aag ttt ctg gat aaa gcg ctg    1008
123 Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu
124             325              330              335
126 gaa gat tac cgc gac gcc cgc aaa ggg ctg gac gat tta gct aaa ccg    1056
127 Glu Asp Tyr Arg Asp Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro
128             340              345              350
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130 agc gag aaa gcc att cac ccg caa tat ctg gcg cag caa att agt cat        1104
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132         355             360             365
134 ttt gcc gcc gat gac gct att ttc acc tgt gac gtt ggt acg cca acg        1152
135 Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr
136         370             375             380
138 gtg tgg gcg gca cgt tat cta aaa atg aac ggc aag cgt cgc ctg tta        1200
139 Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu
140 385             390             395             400
142 ggt tcg ttt aac cac ggt tcg atg gct aac gcc atg ccg cag gcg ctg        1248
143 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Leu
144         405             410             415
146 ggt gcg cag gcg aca gag cca gaa cgt cag gtg gtc gcc atg tgc ggc        1296
147 Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
148         420             425             430
150 gat ggc ggt ttt agc atg ttg atg ggc gat ttc ctc tca gta gtg cag        1344
151 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
152         435             440             445
154 atg aaa ctg cca gtg aaa att gtc gtc ttt aac aac agc gtg ctg ggc        1392
155 Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
156     450             455             460
158 ttt gtg gcg atg gag atg aaa gct ggt ggc tat ttg act gac ggc acc        1440
159 Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
160 465             470             475             480
162 gaa cta cac gac aca aac ttt gcc cgc att gcc gaa gcg tgc ggc att        1488
163 Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
164         485             490             495
166 acg ggt atc cgt gta gaa aaa gcg tct gaa gtt gat gaa gcc ctg caa        1536
167 Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
168         500             505             510
170 cgc gcc ttc tcc atc gac ggt ccg gtg ttg gtg gat gtg gtg gtc gcc        1584
171 Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
172         515             520             525
174 aaa gaa gag tta gcc att cca ccg cag atc aaa ctc gaa cag gcc aaa        1632
175 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
176     530             535             540
178 ggt ttc agc ctg tat atg ctg cgc gca atc atc agc gga cgc ggt gat        1680
179 Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp
180 545             550             555             560
182 gaa gtg atc gaa ctg gcg aaa aca aac tgg cta agg taa                    1719
183 Glu Val Ile Glu Leu Ala Lys Thr Asn Trp Leu Arg
184         565             570
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188 <211> LENGTH: 572
189 <212> TYPE: PRT
190 <213> ORGANISM: Escherichia coli
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195 1           5               10              15
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198 Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu
199             20              25              30
202 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg
203         35              40              45
206 His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser
207     50              55              60
210 Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His
211 65              70              75              80
214 Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu
215             85              90              95
218 Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe
219             100             105             110
222 Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys
223         115             120             125
226 Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala
227     130             135             140
230 Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro
231 145             150             155             160
234 Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp
235             165             170             175
238 Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg
239             180             185             190
242 Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys
243         195             200             205
246 Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly
247     210             215             220
250 Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val
251 225             230             235             240
254 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe
255             245             250             255
258 Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu
259             260             265             270
262 Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile
263         275             280             285
266 Ile Gln Ile Asp Ile Asn Pro Ala Ser Ile Gly Ala His Ser Lys Val
267     290             295             300
270 Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu
271 305             310             315             320
274 Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu
275             325             330             335
278 Glu Asp Tyr Arg Asp Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro
279             340             345             350
282 Ser Glu Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser His
283         355             360             365
286 Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr
287     370             375             380
290 Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu
291 385             390             395             400
294 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Leu
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295                 405               410               415
298 Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
299             420               425               430
302 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
303         435               440               445
306 Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
307     450               455               460
310 Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
311 465               470               475               480
314 Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
315             485               490               495
318 Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
319         500               505               510
322 Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
323         515               520               525
326 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
327     530               535               540
330 Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp
331 545               550               555               560
334 Glu Val Ile Glu Leu Ala Lys Thr Asn Trp Leu Arg
335             565               570
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338 <210> SEQ ID NO: 3
339 <211> LENGTH: 1454
340 <212> TYPE: DNA
341 <213> ORGANISM: Escherichia coli
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (1)..(1454)
346 <223> OTHER INFORMATION: mutagenic DNA
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350 <221> NAME/KEY: misc_feature
351 <222> LOCATION: (1)..(56)
352 <223> OTHER INFORMATION: technical DNA/residue of the polylinker sequence
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (57)..(577)
358 <223> OTHER INFORMATION: part of the 5' region (poxB1) of the poxB gene
361 <220> FEATURE:
362 <221> NAME/KEY: misc_feature
363 <222> LOCATION: (578)..(646)
364 <223> OTHER INFORMATION: technical DNA/residue of the polylinker sequence
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368 <221> NAME/KEY: misc_feature
369 <222> LOCATION: (647)..(1398)
370 <223> OTHER INFORMATION: part of the 3' region (poxB2) of the poxB gene
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374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (1399)..(1454)
376 <223> OTHER INFORMATION: technical DNA/residue of the polylinker sequence

VERIFICATION SUMMARY   DATE: 06/20/2002
PATENT APPLICATION: **US/10/076,416**   TIME: 17:39:05

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